

## SEQUENCE LISTING

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## (1) GENERAL INFORMATION:

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## (i) APPLICANT:

- (A) NAME: Boehringer Ingelheim International GmbH
- (B) STREET: Binger Strasse 173
- (C) CITY: Ingelheim am Rhein
- (E) COUNTRY: Germany
- (F) POSTAL CODE (ZIP): 55216
- (G) TELEPHONE: 06132/772282
- (H) TELEFAX: 06132/774377

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## (ii) TITLE OF INVENTION: Tumor-associated Antigen

## (iii) NUMBER OF SEQUENCES: 28

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## (iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

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## (2) INFORMATION FOR SEQ ID NO: 1:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 679 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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## (ii) MOLECULE TYPE: cDNA to mRNA

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## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

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## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: homo sapiens
- (F) TISSUE TYPE: Melanoma

## (ix) FEATURE:

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- (A) NAME/KEY: 3'UTR

(B) LOCATION:340..679

(ix) FEATURE:

5 (A) NAME/KEY: 5'UTR  
(B) LOCATION:1..9

(ix) FEATURE:

10 (A) NAME/KEY: CDS  
(B) LOCATION:10..339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

15	CGA GGG GCG ATG CTG ATG GGC CAG GAG GGC CTG GCA TTC CTG ATG GGC	48
	Met Leu Met Ala Gln Glu Ala Leu Ala Phe Leu Met Ala	
	1 5 10	
20	CAG GGG GCA ATG CTG GCG GGC CAG GAG AGG GCG GTG CCA GCG GCG GCA	96
	Gln Gly Ala Met Leu Ala Ala Gln Glu Arg Arg Val Pro Arg Ala Ala	
	15 20 25	
25	GAG GTC CCC GGG GCG CAG GGG CAG CAA GGG CCT GCG GGC GCA GAG GAG	144
	Glu Val Pro Gly Ala Gln Gly Gln Gln Gly Pro Arg Gly Arg Glu Glu	
	30 35 40 45	
30	GCG CCC GCG GGG GTC GCG ATG GCG GTG CCG CTT CTG GCG AGG ATG GAA	192
	Ala Pro Arg Gly Val Arg Met Ala Val Pro Leu Leu Arg Arg Met Glu	
	50 55 60	
35	GGT GGC CCT GCG GGG CCA GGA GGC GCG ACA GGC GGC TGC TTC AGT TGC	240
	Gly Ala Pro Ala Gly Pro Gly Gly Arg Thr Ala Ala Cys Phe Ser Cys	
	65 70 75	
40	ACA TCA CGA TGC CTT TCT GGT GCG CCA TGG AAG GCG AGC TGG TCC GCA	288
	Thr Ser Arg Cys Leu Ser Arg Arg Pro Trp Lys Arg Ser Trp Ser Ala	
	80 85 90	
45	GGA TCC TGT CCC GGG ATG CCG CAC CTC TCC CCC GAC CAG GGG GCG TTC	336
	Gly Ser Cys Pro Gly Met Pro His Leu Ser Pro Asp Gln Gly Arg Phe	
	95 100 105	
50	TGA AGGACTTCAC CGTGTCGGC AACCTACTGT TTATCGACT GACTGCTGCA	389
	*	
55	110	
	GACCAAGGOC AACTGCAGCT CTCATCAGC TCTGTCTCC AGCAGCTTTC CCTGTGATG	449
	TGGATCAGC AGTGCTTTCT GCGGTGTTT TTGGCTCAGG CTCCTCAGG GCAGAGGCGC	509
	TAAGGOCAGC CTGGGCGGCC TTCTAGGTC ATGCTCTCTC CCTAGGGAA TGGTCCAGC	569
	ACGAGTGGOC AGTTCATTGT GGGGCGCTGA TTGTTGTGCG CTGGAGGAGG ACGGCTTACA	629
	TGTTGTGTTT TGTAGAAAT AAAGCTGAGC TACGAAAAA AAAAAAAAAA	679

## (2) INFORMATION FOR SEQ ID NO: 2:

5 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 109 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

15 Met Leu Met Ala Gln Glu Ala Leu Ala Phe Leu Met Ala Gln Gly Ala  
 1 5 10 15

Met Leu Ala Ala Gln Glu Arg Arg Val Pro Arg Ala Ala Glu Val Pro  
 20 25 30

20 Gly Ala Gln Gly Gln Gln Gly Pro Arg Gly Arg Glu Glu Ala Pro Arg  
 35 40 45

Gly Val Arg Met Ala Val Pro Leu Leu Arg Arg Met Glu Gly Ala Pro  
 50 55 60

25 Ala Gly Pro Gly Gly Arg Thr Ala Ala Cys Phe Ser Cys Thr Ser Arg  
 65 70 75 80

30 Cys Leu Ser Arg Arg Pro Trp Lys Arg Ser Trp Ser Ala Gly Ser Cys  
 85 90 95

Pro Gly Met Pro His Leu Ser Pro Asp Gln Gly Arg Phe \*  
 100 105 110

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## (2) INFORMATION FOR SEQ ID NO: 3:

40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 767 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

50 (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: homo sapiens  
 (F) TISSUE TYPE: Melanoma

55 (ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 54...596

## (ix) FEATURE:

(A) NAME/KEY: 3'UTR

(B) LOCATION:597..767

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## (ix) FEATURE:

(A) NAME/KEY: 5'UTR

(B) LOCATION:1..53

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

	ATCTCTGGTGG GCGCTGAOCT TCTCTCTGAG AGCGGGGAG AGGCTOOGGA GGC ATG	56
		Met
15		1
	CAG GGC GAA GGC CAG GGC ACA GGG GGT TOG ACG GGC GAT GCT GAT GGC	104
	Gln Ala Glu Gly Gln Gly Thr Gly Gly Ser Thr Gly Asp Ala Asp Gly	
	5 10 15	
20	CCA GGA GGC OCT GGC ATT OCT GAT GGC CCA GGG GGC AAT GCT GGC GGC	152
	Pro Gly Gly Pro Gly Ile Pro Asp Gly Pro Gly Gly Asn Ala Gly Gly	
	20 25 30	
25	CCA GGA GAG GCG GGT GGC ACG GGC GGC AGA GGT CCG CCG GGC GCA GGG	200
	Pro Gly Glu Ala Gly Ala Thr Gly Gly Arg Gly Pro Arg Gly Ala Gly	
	35 40 45	
30	GCA GCA AGG GGC TOG GGG CCG AGA GGA GGC GGC CCG CCG GGT CCG CAT	248
	Ala Ala Arg Ala Ser Gly Pro Arg Gly Gly Ala Pro Arg Gly Pro His	
	50 55 60 65	
	GGC GGT GGC GCT TCT GCG CAG GAT GGA AGG TGC CCG TGC GGG GGC AGG	296
	Gly Gly Ala Ala Ser Ala Gln Asp Gly Arg Cys Pro Cys Gly Ala Arg	
35		70 75 80
	AGG CCG GAC AGC CCG CTG CTT CAG TTG CAC ATC ACG ATG OCT TTC TOG	344
	Arg Pro Asp Ser Arg Leu Leu Gln Leu His Ile Thr Met Pro Phe Ser	
	85 90 95	
40	TOG CCG ATG GAA GCG GAG CTG GTC CCG AGG ATC CTG TOC CCG GAT GGC	392
	Ser Pro Met Glu Ala Glu Leu Val Arg Arg Ile Leu Ser Arg Asp Ala	
	100 105 110	
45	GCA OCT CTC CCG CGA CCA GGG GCG GTT CTG AAG GAC TTC ACC GTG TOC	440
	Ala Pro Leu Pro Arg Pro Gly Ala Val Leu Lys Asp Phe Thr Val Ser	
	115 120 125	
50	GGC AAC CTA CTG TTT ATC CGA CTG ACT GCT GCA GAC CAC CCG CAA CTG	488
	Gly Asn Leu Leu Phe Ile Arg Leu Thr Ala Ala Asp His Arg Gln Leu	
	130 135 140 145	
	CAG CTC TOC ATC AGC TOC TGT CTC CAG CAG CTT TOC CTG TTG ATG TGG	536
	Gln Leu Ser Ile Ser Ser Cys Leu Gln Gln Leu Ser Leu Leu Met Trp	
55		150 155 160

ATC ACG CAG TGC TTT CTG CCC GTG TTT TTG GCT CAG GCT CCC TCA GGG 584  
 Ile Thr Gln Cys Phe Leu Pro Val Phe Leu Ala Gln Ala Pro Ser Gly  
 165 170 175

5 CAG AGG CGC TAA GGCAGGCTG GGGGCGCTTC CTAGGTCATG CCTCTCTCCC 636  
 Gln Arg Arg \*  
 180

10 TAGGGAATGG TOCCAGCAAG AGTGGCCAGT TCATTGTGGG GGCTGATTG TTGTGCGCTG 696  
 GAGGAGGACG GCTTACATGT TTGTTCTGT AGAAAATAAA GCTGAGCTAC GAAAAAAAAA 756  
 AAAAAAAAAA A 767

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(2) INFORMATION FOR SEQ ID NO: 4:

20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 180 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

30 Met Gln Ala Glu Gly Gln Gly Thr Gly Gly Ser Thr Gly Asp Ala Asp 15  
 1 5 10 15  
 Gly Pro Gly Gly Pro Gly Ile Pro Asp Gly Pro Gly Gly Asn Ala Gly 30  
 20 25 30  
 35 Gly Pro Gly Glu Ala Gly Ala Thr Gly Gly Arg Gly Pro Arg Gly Ala 45  
 35 40 45  
 Gly Ala Ala Arg Ala Ser Gly Pro Arg Gly Gly Ala Pro Arg Gly Pro 60  
 40 50 55 60  
 His Gly Gly Ala Ala Ser Ala Gln Asp Gly Arg Cys Pro Cys Gly Ala 80  
 65 70 75 80  
 45 Arg Arg Pro Asp Ser Arg Leu Leu Gln Leu His Ile Thr Met Pro Phe 95  
 85 90 95  
 Ser Ser Pro Met Glu Ala Glu Leu Val Arg Arg Ile Leu Ser Arg Asp 110  
 100 105 110  
 50 Ala Ala Pro Leu Pro Arg Pro Gly Ala Val Leu Lys Asp Phe Thr Val 125  
 115 120 125  
 Ser Gly Asn Leu Leu Phe Ile Arg Leu Thr Ala Ala Asp His Arg Gln 140  
 130 135 140  
 55 Leu Gln Leu Ser Ile Ser Ser Cys Leu Gln Gln Leu Ser Leu Leu Met 160  
 145 150 155 160

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Trp Ile Thr Gln Cys Phe Leu Pro Val Phe Leu Ala Gln Ala Pro Ser  
 165 170 175

5 Gly Gln Arg Arg \*  
 180

10 (2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 993 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: homo sapiens  
 (F) TISSUE TYPE: Melanoma

(ix) FEATURE:

- (A) NAME/KEY: 5'UTR  
 (B) LOCATION:1..55

(ix) FEATURE:

- (A) NAME/KEY: CDS  
 (B) LOCATION:56..688

(ix) FEATURE:

- (A) NAME/KEY: 3'UTR  
 (B) LOCATION:689..993

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

GCATCTCTGT GGGGCTGAC CTCTCTCTG AGAGGCTGAG AGAGGCTGAG GAGGC ATG 58  
 Met  
 1  
 45 CAG GGC GAA GGC CAG GGC ACA GGC GGT TOG ACG GGC GAT GCT GAT GGC 106  
 Gln Ala Glu Gly Gln Gly Thr Gly Gly Ser Thr Gly Asp Ala Asp Gly  
 5 10 15  
 50 CCA GGA GGC OCT GGC ATT OCT GAT GGC CCA GGC GGC AAT GCT GGC GGC 154  
 Pro Gly Gly Pro Gly Ile Pro Asp Gly Pro Gly Gly Asn Ala Gly Gly  
 20 25 30  
 55 CCA GGA GAG GGC GGT GGC ACG GGC GGC AGA GGT CCG CCG GGC CCA GGC 202  
 Pro Gly Glu Ala Gly Ala Thr Gly Gly Arg Gly Pro Arg Gly Ala Gly  
 35 40 45  
 GCA GCA AGG GGC TOG GGC CCG AGA GGA GGC GGC CCG CCG GGT CCG CAT 250

	Ala Ala Arg Ala Ser Gly Pro Arg Gly Gly Ala Pro Arg Gly Pro His	
	50 55 60 65	
5	GGC GGT GGC GCT TCT GCG CAG GAT GGA AGG TGC CCC TGC GGG GGC AGG Gly Gly Ala Ala Ser Ala Gln Asp Gly Arg Cys Pro Cys Gly Ala Arg	298
	70 75 80	
10	AGG CCG GAC AGC CCG CTG CTT CAG TTG CAC ATC ACG ATG OCT TTC TCG Arg Pro Asp Ser Arg Leu Leu Gln Leu His Ile Thr Met Pro Phe Ser	346
	85 90 95	
15	TCG CCC ATG GAA GCG GAG CTG GTC CCG AGG ATC CTG TCC CCG GAT GGC Ser Pro Met Glu Ala Glu Leu Val Arg Arg Ile Leu Ser Arg Asp Ala	394
	100 105 110	
20	GCA OCT CTC CCC CGA CCA GCG GCG GTT CTG AAG GAC TTC ACC GTG TCC Ala Pro Leu Pro Arg Pro Gly Ala Val Leu Lys Asp Phe Thr Val Ser	442
	115 120 125	
25	GGC AAC CTA CTG TTT ATG TCA GTT CCG GAC CAG GAC AGG GAA GGC GCT Gly Asn Leu Leu Phe Met Ser Val Arg Asp Gln Asp Arg Glu Gly Ala	490
	130 135 140 145	
30	GGG CCG ATG AGG GTG GTG GGT TGG GCG CTG GGA TCC GGC TCC CCG GAG Gly Arg Met Arg Val Val Gly Trp Gly Leu Gly Ser Ala Ser Pro Glu	538*
	150 155 160	
35	GGG CAG AAA GCT AGA GAT CTC AGA ACA CCC AAA CAC AAG GTC TCA GAA Gly Gln Lys Ala Arg Asp Leu Arg Thr Pro Lys His Lys Val Ser Glu	586
	165 170 175	
40	CAG AGA OCT GGT ACA CCA GCG CCG CCG CCA CCC GAG GGA GGC CAG GGA Gln Arg Pro Gly Thr Pro Gly Pro Pro Pro Pro Glu Gly Ala Gln Gly	634
	180 185 190	
45	GAT GGG TGC AGA GGT GTC GGC TTT AAT GTG ATG TTC TCT GGC OCT CAC Asp Gly Cys Arg Gly Val Ala Phe Asn Val Met Phe Ser Ala Pro His	682
	195 200 205	
50	ATT TAG CCGACTGACT GCTGCAGACC ACGGCCAACT GCAGCTCTCC ATCAGCTCCT Ile *	738
	210	
55	GCTCCAGCA GCTTTCCCTG TTGATGTGGA TCAAGCAGTG CTTTCTGCCC GIGTTTTTGG	798
	CTCAGGCTCC CTCAGGGCAG AGGCGCTAAG CCGAGCCCTGG CGCCCCCTCC TAGGTCATGC	858
	CTCCTCCCT AGGGAATGGT CCGACCAAGA GTGGCCAGTT CATTGTGGGG GCGTGATTGT	918
	TTGTGCGTGG AGGAGCAAGG CTTACATGTT TGTTTCGTGA GAAAATAAAG CTGAGCTAAG	978
	AAAAAAAAA AAAAA	993

(2) INFORMATION FOR SEQ ID NO: 6:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

10 Met Gln Ala Glu Gly Gln Gly Thr Gly Gly Ser Thr Gly Asp Ala Asp  
     1                    5                    10                    15

Gly Pro Gly Gly Pro Gly Ile Pro Asp Gly Pro Gly Gly Asn Ala Gly  
                     20                    25                    30

15 Gly Pro Gly Glu Ala Gly Ala Thr Gly Gly Arg Gly Pro Arg Gly Ala  
                     35                    40                    45

Gly Ala Ala Arg Ala Ser Gly Pro Arg Gly Gly Ala Pro Arg Gly Pro  
     20            50                    55                    60

His Gly Gly Ala Ala Ser Ala Gln Asp Gly Arg Cys Pro Cys Gly Ala  
     65                    70                    75                    80

25 Arg Arg Pro Asp Ser Arg Leu Leu Gln Leu His Ile Thr Met Pro Phe  
                     85                    90                    95

Ser Ser Pro Met Glu Ala Glu Leu Val Arg Arg Ile Leu Ser Arg Asp  
                     100                    105                    110

30 Ala Ala Pro Leu Pro Arg Pro Gly Ala Val Leu Lys Asp Phe Thr Val  
                     115                    120                    125

Ser Gly Asn Leu Leu Phe Met Ser Val Arg Asp Gln Asp Arg Glu Gly  
     35            130                    135                    140

Ala Gly Arg Met Arg Val Val Gly Trp Gly Leu Gly Ser Ala Ser Pro  
     145                    150                    155                    160

40 Glu Gly Gln Lys Ala Arg Asp Leu Arg Thr Pro Lys His Lys Val Ser  
                     165                    170                    175

Glu Gln Arg Pro Gly Thr Pro Gly Pro Pro Pro Pro Glu Gly Ala Gln  
                     180                    185                    190

45 Gly Asp Gly Cys Arg Gly Val Ala Phe Asn Val Met Phe Ser Ala Pro  
                     195                    200                    205

50 His Ile \*  
     210

55

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:



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(A) LENGTH: 752 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: cDNA to mRNA  
(iii) HYPOTHETICAL: NO  
10 (iv) ANTI-SENSE: NO  
(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens  
15 (ix) FEATURE:  
(A) NAME/KEY: 5'UTR  
(B) LOCATION:1..53  
(ix) FEATURE:  
20 (A) NAME/KEY: CDS  
(B) LOCATION:54..596  
(ix) FEATURE:  
25 (A) NAME/KEY: 3'UTR  
(B) LOCATION:597..752  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

30 ATCTCTGGTGG GGGCTGACCT TCTCTCTGAG AGCGGGGAG AGGCTCGGA GGC ATG 56  
Met  
1  
CAG GGC GAA GGC CGG GGC ACA GGG GGT TCG ACG GGC GAT GCT GAT GGC 104  
Gln Ala Glu Gly Arg Gly Thr Gly Gly Ser Thr Gly Asp Ala Asp Gly  
5 10 15  
CCA GGA GGC CCT GGC ATT OCT GAT GGC CCA GGG GGC AAT GCT GGC GGC 152  
Pro Gly Gly Pro Gly Ile Pro Asp Gly Pro Gly Gly Asn Ala Gly Gly  
20 25 30  
CCA GGA GAG GCG GGT GGC ACG GGC GGC AGA GGT CCC CGG GGC GCA GGC 200  
Pro Gly Glu Ala Gly Ala Thr Gly Gly Arg Gly Pro Arg Gly Ala Gly  
35 40 45  
GCA GCA AGG GGC TCG GGG CCG GGA GGA GGC GGC CCG CCG GGT CCG CAT 248  
Ala Ala Arg Ala Ser Gly Pro Gly Gly Gly Ala Pro Arg Gly Pro His  
50 55 60 65  
GGC GGC GCG GCT TCA GGG CTG AAT GGA TGC TGC AGA TGC GGC GGC AGG 296  
Gly Gly Ala Ala Ser Gly Leu Asn Gly Cys Cys Arg Cys Gly Ala Arg  
70 75 80  
GGG CCG GAG AGC CGC CTG CTT GAG TTC TAC CTC GGC ATG OCT TTC GGC 344  
Gly Pro Glu Ser Arg Leu Leu Glu Phe Tyr Leu Ala Met Pro Phe Ala  
85 90 95  
ACA CCC ATG GAA GCA GAG CTG GGC CGC AGG AGC CTG GGC CAG GAT GGC 392

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Thr Pro Met Glu Ala Glu Leu Ala Arg Arg Ser Leu Ala Gln Asp Ala  
 100 105 110

5 OCA CCG CTT CCC GTG CCA GGG GTG CTT CTG AAG GAG TTC ACT GTG TOC 440  
 Pro Pro Leu Pro Val Pro Gly Val Leu Leu Lys Glu Phe Thr Val Ser  
 115 120 125

10 GGC AAC ATA CTG ACT ATC OGA CTG ACT GCT GCA GAC CAC CGC CAA CTG 488  
 Gly Asn Ile Leu Thr Ile Arg Leu Thr Ala Ala Asp His Arg Gln Leu  
 130 135 140 145

15 CAG CTC TOC ATC AGC TOC TGT CTC CAG CAG CTT TOC CTG TTG ATG TGG 536  
 Gln Leu Ser Ile Ser Ser Cys Leu Gln Gln Leu Ser Leu Leu Met Trp  
 150 155 160

ATC ACG CAG TGC TTT CTG CCC GTG TTT TTG GCT CAG OCT CCC TCA GGG 584  
 Ile Thr Gln Cys Phe Leu Pro Val Phe Leu Ala Gln Pro Pro Ser Gly  
 165 170 175

20 CAG AGG CGC TAA GGCAGGCTG GGGGCGCTTC CTAGGTCATG OCTOCTOCCC 636  
 Gln Arg Arg \*  
 180

25 TAGGGAATGG TOCCAGCAAG AGTGGCCAGT TCATTGIGGG GGCTGATTG TTTGTGCTG 696  
 GAGGAGGACG GCCTACATGT TTGTTCTGCT AGAAAATAAA ACTGAGCTAC GAAAAA 752

30 (2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 180 amino acids  
 35 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Met Gln Ala Glu Gly Arg Gly Thr Gly Gly Ser Thr Gly Asp Ala Asp  
 1 5 10 15

45 Gly Pro Gly Gly Pro Gly Ile Pro Asp Gly Pro Gly Gly Asn Ala Gly  
 20 25 30

Gly Pro Gly Glu Ala Gly Ala Thr Gly Gly Arg Gly Pro Arg Gly Ala  
 35 40 45

50 Gly Ala Ala Arg Ala Ser Gly Pro Gly Gly Gly Ala Pro Arg Gly Pro  
 50 55 60

55 His Gly Gly Ala Ala Ser Gly Leu Asn Gly Cys Cys Arg Cys Gly Ala  
 65 70 75 80

Arg Gly Pro Glu Ser Arg Leu Leu Glu Phe Tyr Leu Ala Met Pro Phe  
 85 90 95

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Ala Thr Pro Met Glu Ala Glu Leu Ala Arg Arg Ser Leu Ala Gln Asp  
                   100                  105                  110

5 Ala Pro Pro Leu Pro Val Pro Gly Val Leu Leu Lys Glu Phe Thr Val  
                   115                  120                  125

Ser Gly Asn Ile Leu Thr Ile Arg Leu Thr Ala Ala Asp His Arg Gln  
           130                  135                  140

10 Leu Gln Leu Ser Ile Ser Ser Cys Leu Gln Gln Leu Ser Leu Leu Met  
      145                  150                  155                  160

15 Trp Ile Thr Gln Cys Phe Leu Pro Val Phe Leu Ala Gln Pro Pro Ser  
                   165                  170                  175

Gly Gln Arg Arg \*  
           180

20

## (2) INFORMATION FOR SEQ ID NO: 9:

25 (i) SEQUENCE CHARACTERISTICS:  
       (A) LENGTH: 752 base pairs  
       (B) TYPE: nucleic acid  
       (C) STRANDEDNESS: single  
       (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

35

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: homo sapiens

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(ix) FEATURE:

(A) NAME/KEY: 5'UTR

(B) LOCATION:1..93

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(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION:94..270

50

(ix) FEATURE:

(A) NAME/KEY: 3'UTR

(B) LOCATION:271..752

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

55 ATCTCTGTGG GCGCTGACCT TCTCTCTGAG AGCGGGGCGAG AGGCTCGGA GCCATGCAGG 60

CCGAGGCGCG GGGCAGAGGG GGTTGAGCGG GCG ATG CTG ATG GCC CAG GAG GCC 114

Met Leu Met Ala Gln Glu Ala

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		1	5	
	CTG GCA TTC CTG ATG GGC CAG GGG GCA ATG CTG GCG GGC CAG GAG AGG			162
5	Leu Ala Phe Leu Met Ala Gln Gly Ala Met Leu Ala Ala Gln Glu Arg	10	15	20
	CGG GTG CCA GCG GCG GCA GAG GTC CCC GGG GCG CAG GGG CAG CAA GGG			210
10	Arg Val Pro Arg Ala Ala Glu Val Pro Gly Ala Gln Gly Gln Gln Gly	25	30	35
	CCG GGC GCG GAG GAG GCG CCC GCG GGG GTC GCG ATG GCG GCG GCG			258
	Pro Arg Gly Arg Glu Glu Ala Pro Arg Gly Val Arg Met Ala Ala Arg	40	45	50
				55
15	CTT CAG GGC TGA ATGGATGCTG CAGATGCGGG GGCAGGGGGC GCGAGAGGCG			310
	Leu Gln Gly *			
	CCGCTGTGAG TTCTAAGCTG CCATGCTTTT CGGACAAOC ATGGAAGCAG AGCTGGGCGG			370
20	CAGGAGGCTG GGCAGGATG CCCCACCGCT TCCCGTGCCA GGGGTGCTTC TGAAGGAGTT			430
	CACGTGTGCC GGCAACATAC TGAATATCG ACTGACTGCT GCAGACCAOC GCGAAGTGCA			490
25	GCCTTCATC AGCTCTGTC TCCAGCAGCT TTCCCTGTG ATGTTGATCA GCGATGCTT			550
	TCGCGCGTG TTTTGTGCTC AGCTCCCTC AGGGCAGAGG CGCTAAGGOC AGCTGGGCG			610
30	CCCTCTAG GTCATGCTC CTCCCTAGG GAATGGTCC AGCAAGAGTG GCGATTAT			670
	TGCGGGGCG TGATGTGTTG TGCTGGAGG AGGACGGCTT ACATGTTTGT TTCTGTAGAA			730
	AATAAACTG AGCTAGAAA AA			752
35				

(2) INFORMATION FOR SEQ ID NO: 10:

- 40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 58 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear
- 45 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Met Leu Met Ala Gln Glu Ala Leu Ala Phe Leu Met Ala Gln Gly Ala  
 1 5 10 15  
 5 Met Leu Ala Ala Gln Glu Arg Arg Val Pro Arg Ala Ala Glu Val Pro  
 20 25 30  
 10 Gly Ala Gln Gly Gln Gln Gly Pro Arg Gly Arg Glu Glu Ala Pro Arg  
 35 40 45  
 Gly Val Arg Met Ala Ala Arg Leu Gln Gly \*

15

2) INFORMATION FOR SEQ ID NO: 11:

20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 11 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

30 Met Leu Met Ala Gln Glu Ala Leu Ala Phe Leu  
 1 5 10....

35 2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 10 amino acids  
 (B) TYPE: amino acid  
 40 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

45 Leu Met Ala Gln Glu Ala Leu Ala Phe Leu  
 1 5 10.

50

(2) INFORMATION FOR SEQ ID NO: 13:

55 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 21 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: synthetic DNA

5 GGTGACACTA TAGAAGGTAC G 21

10 (2) INFORMATION FOR SEQ ID NO: 14:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: synthetic DNA

20 TGATGTGCAA CTGAAGCAGG.....20

25 (2) INFORMATION FOR SEQ ID NO: 15:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 21 base pairs  
 (B) TYPE: nucleic acid  
 30 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: synthetic DNA

35 GCACTGCGTG ATCCACATCA A 21

40 (2) INFORMATION FOR SEQ ID NO: 16:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 21 base pairs  
 (B) TYPE: nucleic acid  
 45 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: synthetic DNA

50 CGACTCACTA TAGGTAGAGA G 21

## (2) INFORMATION FOR SEQ ID NO: 17:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

5

## 10 (ii) MOLECULE TYPE: synthetic DNA

GCACATCAG ATGCTTTTCT CGTGG

25

15

## (2) INFORMATION FOR SEQ ID NO: 18:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 32 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

20

## 25 (ii) MOLECULE TYPE: synthetic DNA

CACACAAAGC TTGGCTTAGC GCCTCTGCCC TG.....32

30

## (2) INFORMATION FOR SEQ ID NO: 19:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 30 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

35

## 40 (ii) MOLECULE TYPE: synthetic DNA

CACACAGGAT CCATGGATGC TGCAGATGG.....30

45

## (2) INFORMATION FOR SEQ ID NO: 20:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

50

## 55 (ii) MOLECULE TYPE: synthetic DNA

GAAGAACATA TGCTGATGGC CCAGGAGGC

29

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: synthetic DNA

TTAAAGATCT CAGAACCGCC OCTGGTCG

28

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: synthetic DNA

ttactogaga tgctgatggc ccagg.....25

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: synthetic DNA

aaggtaacctt gaacogcccc tggtag .....26

2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

Phe Leu Met Ala Gln Gly Ala Met Leu  
1 5 9

5

2) INFORMATION FOR SEQ ID NO: 25:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

20 Ala Met Leu Ala Ala Gln Glu Arg Arg Val  
1 5 10

25

2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9 amino acids

30

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Met Leu Ala Ala Gln Glu Arg Arg Val  
1 5 9

40

2) INFORMATION FOR SEQ ID NO: 27:

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

50

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

55 Tyr Tyr Met Asn Gly Thr Met Ser Gln Val  
1 5 10

WO 00/23584

PCT/EP99/07832

18/18

2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:

5

(A) LENGTH: 9 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

Glu Val Asp Pro Ile Gly His Leu Tyr

1

5

9

15